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Fuscoporia atlantica sp. nov., a new polypore from the Brazilian Atlantic Rainforest

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Abstract — *Fuscoporia atlantica* (*Basidiomycota, Hymenochaetaceae*) is described and illustrated based on specimens collected in Atlantic Rainforest areas of São Paulo state, Brazil, and its inferred phylogenetic relationships are based on sequence data from the ribosomal ITS and LSU regions. The new species is characterized by an effused-reflexed to pileate basidioma, golden-yellow-ferruginous pore surface, tiny pores, dimitic hyphal system with thin-walled hyphae encrusted at dissepiment edges, mostly uncinate or hooked hymenial setae, and broadly ellipsoid to ellipsoid basidiospores. An identification key to the *Fuscoporia* species recorded from Brazil is also provided.

Key words — basidiomycete, *Hymenochaetales*, neotropics, phylogeny, taxonomy

Introduction

Species of the genus *Fuscoporia* Murrill traditionally have been included in *Phellinus* s.l., a morphologically heterogeneous and phylogenetically polyphyletic group (Fiasson & Niemelä 1984; Dai 1999; Wagner & Fischer 2001, 2002b; Larsson et al. 2006). However, molecular phylogenetic analyses have shown that *Fuscoporia* species form a clade independent from *Phellinus* s.s. (Wagner & Fischer 2002b, Larsson et al. 2006).

Fuscoporia was described to accommodate species with resupinate to pileate basidiomes occurring principally on coniferous and deciduous trees characterized by monomitic to dimitic hyphal system, encrusted generative hyphae at the dissepiments (considered diagnostic within *Phellinus* s.l.), hymenial setae, and cylindric to ellipsoid, hyaline, inamyloid, nondextrinoid, thin-walled, smooth basidiospores (Murrill 1907; Fiasson & Niemelä 1984; Dai 1999, 2010; Niemelä et al. 2001; Wagner & Fischer 2001).

Table 1. ITS dataset of *Fuscoporia* and *Phellinidium* spp. used in the phylogenetic analyses.

Species	Voucher specimens	GenBank accession numbers
Fuscoporia atlantica	SP445618 (holotype)	KP058515 {m}
	SP465829 (paratype)	KP058514 {m}
F. callimorpha	JV090487	JF692190 {l}
	JV090487	JF692191 {l}
	JV040914J	JF692193 {l}
F. contigua	JV1007/3	JQ794546 {l}
	JV0907/2[a]	JQ794547 {l}
	JV0309/118	JQ794548 {l}
	JV0309/171	JQ794550 {l}
F. ferrea	CBS 444.48	AY558617 {f}
	D4-3B-b	DQ516525 {i}
	DLL2009-080	JQ673178 {b}
	SP5108	KJ677120 {k}
F. ferruginosa	JV0202/2	J794572 {l}
	JV8909/74	JQ794573 {l}
	JV1109/24	JQ794577 {l}
F. gilva	KCTC 6653	AY558620 {f}
	xsd08128	FJ481039 {e}
	SACCR 11076	JX427049 {d}
	ASIS24343	KF692068 {j}
F. rufitincta (Cooke) Murrill	PRM915961	GU594160 {j}
	JV0610/14PK	JQ794579 {l}
	JV0610/14PK	JQ794580 {j}
F. senex	CBS 442.76	AY558647 {f}
	KUC20110922-13	JX463658 {e}
	Q32	KC414230 {f}
F. torulosa (Pers.) T. Wagner & M. Fisch.	Pt134	EF068139 {c}
	Pt6	EF068238 {h}
	Pt7	EF068239 {h}
F. viticola (Schwein.) Murrill	CBS 381.82	AY558653 {f}
		JQ358814 {a}
	JV0709/163	JQ794583 {l}
Phellinidium sulphurascens	Type 10	EF527215 {g}
	Type 11	EF527216 {g}
P. weirii	CFS504	AY829341 {f}
	CFS586	AY829342 {f}

Sources for published sequences: {a}= Alfredsen et al. (GenBank, unpublished); {b}= Brazee et al. (2012); {c}= Campanile et al. (GenBank, unpublished); {d}= Cantrell et al. (2013); {e}= Jang et al. (2012); {f} = Jeong et al. (GenBank, unpublished); {g} = Lim et al. (2005); {h} = Lim et al. (2008); {i} = Lim et al. (GenBank, unpublished); {j} = Seok et al. (GenBank, unpublished); {k} = Spirin et al. (GenBank, unpublished); {l} = Vlasák et al. (GenBank, unpublished); and {m}= new sequences provided by this study.

Of the approximately 50 species worldwide currently accepted in *Fuscoporia* (Mycobank 2014), 13 have been reported in Brazil, mostly from the Atlantic Rainforest (Baltazar et al. 2009): *F. bifurcata* Baltazar et al., *F. callimorpha* (Lév.) Groposo et al., *F. contigua* (Pers.) G. Cunn., *F. chrysea* (Lév.) Baltazar & Gibertoni, *F. ferrea* (Pers.) G. Cunn., *F. ferruginosa* (Schrad.) Murrill, *F. flavomarginata* (Murrill) Groposo et al., *F. gilva* (Schwein.) T. Wagner & M. Fisch., *F. palmicola* (Berk. & M.A. Curtis) Bondartseva & S. Herrera, *F. punctatiformis* (Murrill) Zmitr. et al., *F. rhabarbarina* (Berk.) Groposo et al., *F. senex* (Nees & Mont.) Ghob.-Nejh., and *F. wahlbergii* (Fr.) T. Wagner & M. Fisch.

During the study of wood-inhabiting fungi in Atlantic Rainforest areas of São Paulo state, an unknown *Fuscoporia* species was found. The phylogeny inferred from ribosomal ITS and LSU sequence analyses of the unknown fungus support it in a monophyletic terminal clade, distinct from all the other *Fuscoporia* species for which DNA sequence data are available, and we describe species here as *F. atlantica*.

Materials & methods

Morphological study

Specimens collected during 2012–2013 in Atlantic Rainforest areas in the São Paulo state, Brazil, were examined according to Gilbertson & Ryvarden (1986) and Núñez & Ryvarden (2001). Basidioma colors are described according to Küppers (2002). For microscopic analysis, free hand sections of the basidiomata were mounted on microscope slides with a drop of 3% KOH solution and 1% aqueous phloxine solution. Amyloid and dextrinoid reactions were observed in Melzer's reagent. Drawings of the microstructures were made with the aid of camera lucida. Thirty basidiospores from each specimen were measured. Abbreviations and codes used for the measurements are: *Dm* = diameter means, $L \times W$ = length mean × width mean, *Q* = range of length/width ratios, *Qm* = length/width mean, and *n* = x/y (x = number of measurements of a given number (y) of specimens) (Coelho 2005). The specimens were deposited in Herbário, Instituto de Botânica, São Paulo, Brazil (SP).

Sequencing

Total DNA was extracted from dried basidiomata. Extractions were carried out using the Sigma-Aldrich Gen Elute™ Plant Genomic DNA Miniprep Kit and later amplified with Sigma-Aldrich ReadyMix™ Taq PCR P4600 (Sigma-Aldrich Corporation, St. Louis, MO, USA), following the manufacturer's recommendations. Primers pairs used were ITS1 and ITS4 for the ITS region (including ITS1, 5.8S and ITS2) and LR0R and LR7 for nLSU (White et al. 1990). Reactions were amplified in a thermal cycler (C1000 Touch™ Thermal Cycler Bio-Rad) using the following parameters: 1 cycle at 94°C for 2 min; 5 cycles at 94°C for 45 s, 60°C for 50 s and 72°C for 1 min and 20 s where the annealing temperature decreases 1°C each cycle until it reaches 56°C under the touch-down technique (Korbie & Mattick 2008); 30 cycles at 95°C for 45 s, 55°C for 50 s, 72°C for 1 min and 20 s; and 72°C for 10 min. PCR products were checked on 2% agarose gel before sequencing and then sequenced in both directions using the same

Table 2. LSU dataset of *Fuscoporia* and related genera used in the phylogenetic analyses.

Species	Voucher specimens	GenBank accession numbers
Coltricia cinnamomea (Jacq.) Murrill	2464 REG	AF311003{s}
Coltricia montagnei (Fr.) Murrill	MF 96-96 REG	AY039683{t}
Coltricia perennis (L.) Murrill	MF 92-96 REG	AF311004{s}
Coltriciella baoshanensis Y.C. Dai & B.K. Cui	Dai 13075 BJFC	KC857267{o}
Coltriciella dependens (Berk. & M.A. Curtis) Murrill	LR 39016 O	AY059059{u}
Coltriciella oblectabilis (Lloyd) Kotl. et al.	RC 11835 O	AY059061{u}
Fomitiporella umbrinella (Bres.) Murrill	CBS 303.66	AY059036{u}
Fomitiporia mediterranea M. Fisch.	FMG3	AY621000{r}
Fomitiporia punctata (P. Karst.) Murrill	MF 85-74 REG	AF311007{s}
Fomitiporia robusta (P. Karst.) Fiasson & Niemelä	TW 242 REG	AF311008{s}
Fulvifomes fastuosus (Lév.) Bondartseva & S. Herrera	CBS 213.36	AY059057{u}
Fulvifomes robiniae (Murrill) Murrill	CBS 211.36	AY059038{u}
Fuscoporia atlantica	SP465829 (paratype)	KP058516{m}
	SP445618 (holotype)	KP058517{m}
Fuscoporia contigua	TW 699 REG	AF311029{s}
Fuscoporia ferrea	MF 87-8 REG	AF311030{s}
Fuscoporia ferruginosa	MF 82-930 REG	AF311032{s}
Fuscoporia gilva	MF 91-42e REG	AY059025{u}
Fuscoporia wahlbergii	MF 89-922	AF311045{s}
Hymenochaete cyclolamellata T. Wagner & M. Fisch.	Cui 8548	JQ279630{n}
Hymenochaete innexa G. Cunn.	He 555	JQ279674{n}
Hymenochaete tropica S.H. He & Y.C. Dai	He 493	JQ279677{n}
Inocutis dryophila (Berk.) Fiasson & Niemelä	MF 87-918 REG	AF311012{s}
Inocutis jamaicensis (Murrill) A.M. Gottlieb et al.	Gilb. 14740 O	AY059048{u}
Inocutis tamaricis (Pat.) Fiasson & Niemelä	MF 96-415 REG	AF311021{s}
Inonotus cuticularis (Bull.) P. Karst.	MF 97-97 REG	AF311010{s}
Inonotus hispidus (Bull.) P. Karst.	MF 92-829 REG	AF311014{s}
Inonotus linteus (Berk. & M.A. Curtis) Teixeira	TAA 84-12 TAA	AY059018{u}
Inonotus obliquus (Ach. ex Pers.) Pilát	TW 705 REG	AF311017{s}
Inonotus tropicalis (M.J. Larsen & Lombard) T. Wagner & M. Fisch.	CBS 617.89	AY059037{u}
Inonotus vaninii (Ljub.) T. Wagner & M. Fisch.	Dai 1980 REG	AY059056{u}
Mensularia crocitincta (Berk & M.A. Curtis) T. Wagner & M. Fisch.	LR 41826 O	AY059043{u}
Mensularia hastifera (Pouzar) T. Wagner & M. Fisch.	MF 84-1023a REG	AF311013{s}
Mensularia radiata (Sowerby) Lázaro Ibiza	TW 704 REG	AF311018{s}
Onnia tomentosa (Fr.) P. Karst.	TW 445 REG	AF311023{s}
Onnia triquetra (Pers.) Imazeki	TW 411 REG	AF311024{s}
Phellinidium ferrugineofuscum (P. Karst.) Fiasson & Niemelä	TN 6121 REG	AF311031{s}

Phellinidium fragrans	CBS 202.90	AY059027{u}
Phellinus arctostaphyli (Long) Niemelä	MF 91-329a REG	AY059026{u}
Phellinus cinereus (Niemelä) M. Fisch.	MF 85-917 REG	AF311027{s}
Phellinus igniarius (L.) Quél.	MF 83-1110a REG	AF311033{s}
Phellinus laevigatus (P. Karst.) Bourdot & Galzin	TN 3260 REG	AF311034{s}
Phellinus overholtsii Ginns	CBS 169.55	AY059019{u}
Phellinus spiculosus (W.A. Campb. & R.W. Davidson) Niemelä	CBS 345.63	AY059055{u}
Phylloporia chrysites (Berk.) Ryvarden	N.W. Legon O	AF411821{v}
Phylloporia pectinata (Klotzsch) Ryvarden	R. Coveny 113 O	AF411823{v}
Phylloporia spathulata (Hook.) Ryvarden	Chay 456 O	AF411822{v}
Bondarzewia montana	SARs.n. 25S	AF042646{q}
Russula violacea		AF218559{p}
Stereum hirsutum	TW 235 REG	AF385165{u}

Sources for published sequences: {n} = He & Dai (2012); {o} = Dai & Cui (GenBank, unpublished); {p} = Miller et al. (2001); {q} = Moncalvo et al. (2000); {r} = Pilotti et al. (2005); {s} = Wagner & Fischer (2001); {t} = Wagner & Fischer (2002a); {u} = Wagner & Fischer (2002b); {v} = Wagner et al. (2002); and {m} = new sequences provided by this study.

primers as the amplification. Nucleotide sequences were determined using an Applied Biosystems 3730xl DNA Analyser (Macrogen, Korea). Edited sequences have been deposited in GenBank (Tables 1, 2).

Phylogenetic analyses

All sequences were matched against the entire GenBank database using BLAST (http://blast.ncbi.nlm.nih.gov/), and their pairwise identity was recorded. Sequences retrieved from GenBank (NCBI) included in the study were selected based on the quality, identity, length, and alignment test to build the ingroup. The selected outgroup for ITS analyses was *Phellinidium fragrans* (M.J. Larsen & Lombard) M. Fisch., *P. weirii* (Murrill) Y.C. Dai, and *P. sulphurascens* (Pilát) Y.C. Dai, based on the results of the LSU region that places *Phellinidium* as a sister group of *Fuscoporia;* the outgroup for LSU analyses was *Bondarzewia montana* (Quél.) Singer, *Russula violacea* Quél., and *Stereum hirsutum* (Willd.) Pers. (based on Wagner & Fischer 2002b). Vouchers and sequences used in this study are provided in Tables 1–2.

The LSU dataset comprising sequences of species in *Hymenochaetaceae* was selected to assess the relative position of the new taxon within the family, while an ITS dataset was assembled to verify placement of the new species among closely related taxa present in GenBank. Nucleotide sequences were aligned automatically with MAFFT v.7 (http://mafft.cbrc.jp/aligment/server/), and then optimized manually with BioEdit 7.2.0 (Hall 1999). Best models of evolution were estimated by using JModeltest 2.c1.4 (Darriba et al. 2012). Substitution models were TrN+I+G in the LSU and TVM+G for the ITS dataset. Bayesian analysis was performed based on independent Markov chain Monte Carlo (MCMC). The run consisted of five million generations, two independent runs, and four independent chains. The sampling frequency was every 500 generations. The first ten percent of the analysis (burn-in phase) was discarded. Posterior probabilities (PP) were determined in MrBayes 3.2.2 (Ronquist et al. 2012) to test the support of the branches' nodes. PP values ≥0.95 were considered statistically significant, and all

branches supported below this value were disregarded. Maximum likelihood (ML) analysis was performed using RaxML 7.5.4-standard (Stamatakis 2006) with 1000 rapid bootstrap replicates. Trees from ML analysis were compared with those resulting from the Bayesian analysis and bootstrap values >50% were used to support the respective nodes compatible between two trees.

Results & discussion

Taxonomy

Fuscoporia atlantica Motato-Vásquez, R.M. Pires & Gugliotta, **sp. nov.** Figs 1–9

MycoBank MB 810911

Differs from *Fuscoporia gilva* by its dark brown crust at the pileus base, its golden-yellow-ferruginous pore surface, its hooked setae, and its larger basidiospores.

Type: Brazil. São Paulo state: Parque Estadual da Cantareira, 23º32′36″S 46º37′59″W, 27 June 2012, V. Motato-Vásquez, M.C. Westphalen & A.C. Bolaños 230 (**Holotype**, SP445618; GenBank KP058515, KP058517).

Etymology: *atlantica* – refers to the Brazilian Atlantic Rainforest biome, the only known habitat of this species.

Basidioma annual, pileate, sessile to effuse-reflexed, flexible when fresh to leathery when dry, solitary to imbricate, without odor or taste. Pileus broadly attached, semicircular, applanate, ≤(5.0–)8.0–9.0 × 4.0–6.0 × 0.1–0.4 cm; upper surface concentrically zonate, radially wrinkled, glabrous to tomentose, brown ($N_{60}A_{90}M_{60}$) to yellowish-brown ($N_{20}A_{90}M_{50}$), with a matte dark brown crust ($N_{50}A_{99}M_{99}$) at the base. Margin thin, obtuse, entire, not involute when dry, sterile, up to 0.2 cm, yellowish-brown ($N_{20}A_{90}M_{50}$) to black brown ($N_{90}M_{99}C_{99}$). Context homogeneous, dense, azonate, golden-yellow-ferruginous ($N_{30}A_{99}M_{30}$). Pore surface golden-yellow-ferruginous ($N_{30}A_{99}M_{30}$), pores rounded, invisible to the naked eye, 7–9 per mm, tubes concolor with the pore surface, ≤0.2 cm deep, dissepiments entire to slightly lacerated, thin to slightly thick. Hyphal system dimitic, generative hypha simple-septate, hyaline, golden yellow to rusty brown, thin to thick-walled, straight, sparsely branched, 3.0–6.5 µm diam., rarely branched, thin-walled hyphae at dissepiments edges encrusted; skeletal hyphae thick-walled, straight, unbranched, dark-brown, 3.0–6.0 µm. Hymenial setae abundant, subulate to ventricose, mostly uncinate or hooked, dark brown and thick-walled, 20–45 × 7–10 µm. Cystidioles abundant. Basidia clavate, hyaline, 4-sterigmated, thin-walled, 9–11 × 5–7 µm. Basidiospores abundant, broadly ellipsoid to ellipsoid, hyaline to pale yellow, smooth, thin-walled, inamyloid, 4–4.5 × (2–)3–3.5 µm (*Xm* = 4.2 × 2.8 µm), *n* = 60/2, *Q* = (1.1–)1.3–2, *Qm* = 1.5.

Ecology & distribution: growing on dead branches and trunks of angiosperms. Known only from Brazilian Atlantic Rainforest, São Paulo state.

Figures 1–4. *Fuscoporia atlantica* (Holotype, SP445618): 1. Basidioma. 2. Margin when dry. 3. Crust on upper surface. 4. Hymenial surface. Scale bars: 1 = 5 cm; 2, 3 = 0.1 cm; 4 = 0.05 cm.

Additional specimens examined —***Fuscoporia atlantica*: BRAZIL. São Paulo state**: Parque Estadual da Serra do Mar, Núcleo Santa Virginia, 11 May 2013, R.M. Pires 8 (SP465829; GenBank KP058514, KPKP058516).

***Fuscoporia gilva*: BRAZIL. São Paulo state**: Parque Estadual da Cantareira, 21 October 2011, V. Motato-Vásquez & A.M. Gugliotta 22 (SP417971); 16 February 2012, M. Capelari & J.J.S. Oliveira 4683 (SP445350).

***Fuscoporia rhabarbarina*: BRAZIL. Santa Catarina state**: 26 December 1988, F. Furlani & C.L. Leite 186 (FLOR 10929). **CANADA**. on wood, Dr. Richardson 4 (K187843, lectotype).

Comments — *Fuscoporia atlantica* is a distinct species that produces effused-reflexed/pileate basidiomata with a radially wrinkled and tomentose pileus and matte dark brown crust at the base, a margin that is yellowish-brown when fresh to black brown after drying, tiny pores, hooked hymenial setae, and broadly ellipsoid to ellipsoid basidiospores. *Fuscoporia atlantica* is very similar to *F. gilva*, which differs microscopically by its straight setae and smaller basidiospores and macroscopically by its crust-less pileus base and

dark purplish brown pore surface (Ryvarden & Johansen 1980, Loguercio-Leite & Wright 1995, Dai 1999). *Fuscoporia wahlbergii*, another effuse-reflexed to pileate species with hooked hymenial setae that occurs in Brazil, can be easily distinguished macroscopically by its woody basidiomata with a reddish-brown to umber upper surface that is narrowly banded in concentric sulcate to flat zones and rusty to chestnut brown pore surface. *Fuscoporia atlantica* is also morphologically similar to *F. rhabarbarina*, which can be easily distinguished macroscopically by a glabrous pileus with sulcate zones and distinctive black crust covering the entire pileus surface and its yellowish brown context and microscopically by the smaller basidiospores (3–4 × 2–3 µm) and straight ventricose hymenial setae (Groposo et al. 2007).

Key to species of *Fuscoporia* from Brazil

1. Basidioma completely resupinate 2
1. Basidioma effused-reflexed to pileate 5

2. Tramal setae present, spores ellipsoid 3
2. Tramal setae absent, spores cylindrical 4

3. Pores 2–3 per mm, hymenial setae subulate ..... *F. contigua*
3. Pores 5–6 per mm, hymenial setae ventricose ..... *F. ferruginosa*

4. Basidioma dark reddish-brown, hymenial setae 18.0–36.0 × 5.0–8.0 µm, basidiospores cylindric, 4.0–7.0 × 2.0–3.0 µm ..... *F. ferrea*
4. Basidioma pale yellow to brown, hymenial setae 10.0–15.0 × 5.0–7.5 µm, basidiospores ellipsoid, 4.5–7.0 × 2–2.5 µm ..... *F. punctatiformis*

5. Pileus with distinct black crust ..... *F. rhabarbarina*
5. Pileus without a black crust 6

6. Hymenial setae bifurcate or spiny ..... *F. bifurcata*
6. Hymenial setae nor bifurcate neither spiny (all setae apically regular) 7

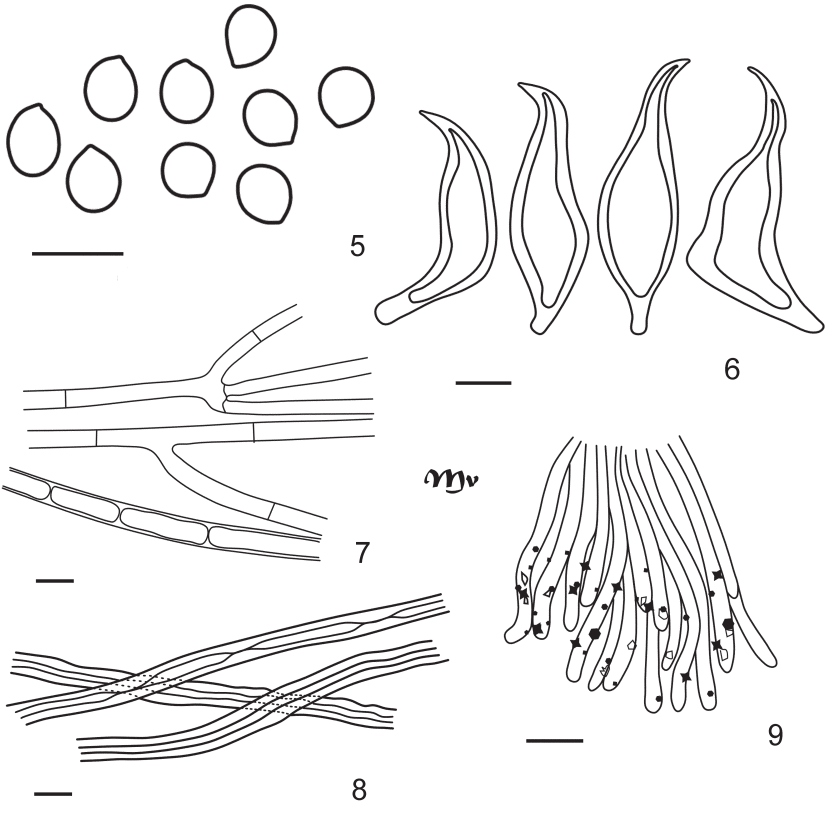
7. Hymenial setae hooked to straight, both present 8
7. Hymenial setae only straight 9

8. Basidioma woody, upper surface without a crust, basidiospores subglobose, 4.0–5.0 × 3.5–4.5 µm ..... *F. wahlbergii*
8. Basidioma leathery, upper surface with a dark brown crust, basidiospores ellipsoid to broadly ellipsoid, 4.0–4.5 × 2.0–3.5 µm .... *F. atlantica*

9. Pores 1–3 per mm ..... *F. palmicola*
9. Pores larger, >4 per mm 10

10. Pores 5–7 per mm 11
10. Pores 8–11 per mm 13

11. Context reddish-brown, basidiospores 2.0–2.5 µm wide ..... *F. chrysea*
11. Context yellowish brown, basidiospores 3.0–3.5 µm wide 12



Figures 5–9. *Fuscoporia atlantica* (from the holotype): 5. Basidiospores. 6. Hymenial setae. 7. Generative hyphae. 8. Skeletal hyphae. 9. Hyphal tips at dissepiment edges. Scale bar = 5 μm.

12. Basidiospores ellipsoid to ovoid, 4.0–5.0 × 3.0–3.5 μm, hymenial setae 20–30 × 5–6 μm ..... *F. gilva*
12. Basidiospores ellipsoid, 3.0–4.5 × 2.5–3.0 μm, hymenial setae 15–30 × 4.5–7.5 μm ..... *F. flavomarginata*
13. Basidiospores ellipsoid to subcylindrical, 3.5–4.5 × 2–3 μm ..... *F. callimorpha*
13. Basidiospores broadly ellipsoid, 4.5–6 × 3.5–5 μm ..... *F. senex*

Phylogenetic analyses

The final LSU matrix comprised 51 sequences and 838 characters, of which 534 (63.72%) were parsimony-informative. Bayesian analysis produced an average standard deviation of split frequencies = 0.003721. The phylogeny

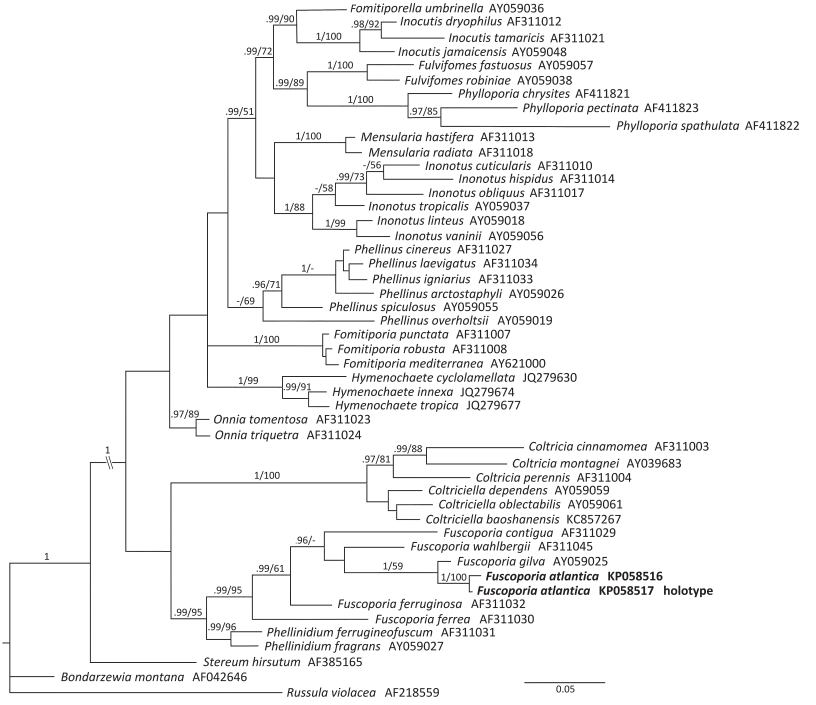


FIGURE 10. Phylogenetic placement of nLSU sequences from *Fuscoporia atlantica* and related species and genera, inferred from Bayesian analysis and ML. The new species is presented in bold font. Support values consist of the Bayesian posterior probability (PP) >0.95, followed by ML bootstrap (BS) values >50%.

derived from LSU sequences of different taxa of *Hymenochaetaceae* from GenBank (FIG. 10) clusters the new species within *Fuscoporia* genus with full support.

The ITS analysis included 37 sequences and 585 characters, of which 302 (51.62%) were parsimony-informative. Bayesian analysis produced an average standard deviation of split frequencies = 0.005049. The ITS-derived tree (FIG. 11) recovered the newly described taxon among a limited number of the most closely related taxa within *Fuscoporia* and supported separation of the new species, *F. atlantica* (PP = 1; bootstrap = 100%). Our morphological and phylogenetic analyses indicated a close relationship between *F. atlantica* and *F. gilva*.

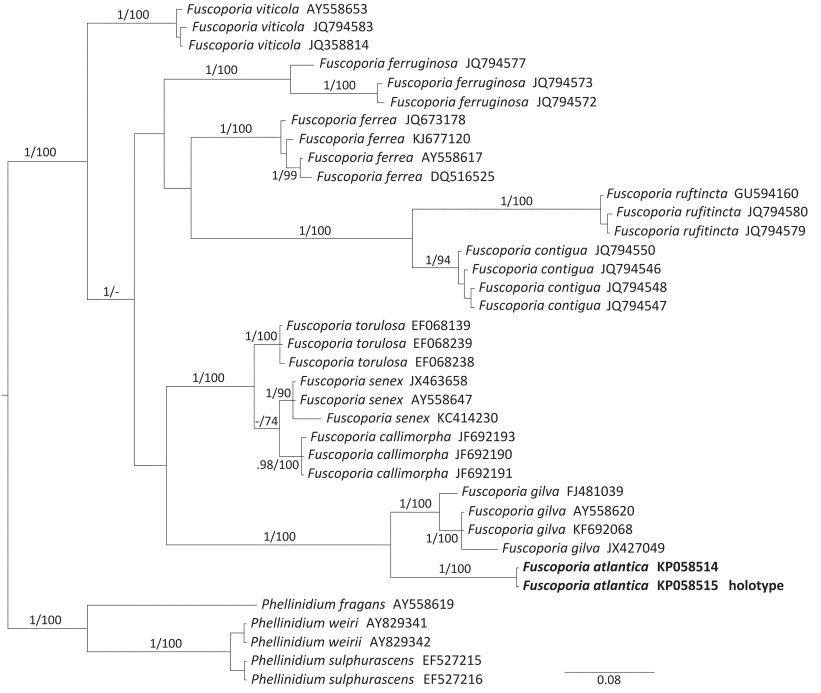


Figure 11. Phylogenetic analysis of ITS sequences from *Fuscoporia atlantica* and related species, based on Bayesian analysis and ML. The new species is presented in bold font. Support values consist of Bayesian posterior probability (PP) values >0.95, followed by ML bootstrap (BS) values >50%.

Our introduction of a new taxon from the Brazilian Atlantic Rainforest, São Paulo, Brazil, offers another example of how poorly known is the fungal diversity in the area.

Acknowledgments

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